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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 15:39:24 ; Search time 101 Seconds
(without alignments)
527.989 Million cell updates/sec

Title: US-10-791-367-1

Perfect score: 30

Sequence: 1 caggcuacgogtagcaucatgccugt 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCYUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	3	US-09-859-724-1
2	30	100.0	31	3	US-09-246-461-3
3	30	100.0	31	3	US-10-021-330-3
4	19.6	65.3	606	3	US-09-270-767-11347
5	19.6	65.3	615	3	US-09-270-767-14489
6	19.6	65.3	705	3	US-09-270-767-10626
7	19.6	65.3	167708	3	US-09-949-016-16423
8	18	62.7	603	3	US-09-489-039A-2715
9	18.8	62.7	1920	3	US-09-447-497-4
10	18.8	62.7	1932	3	US-09-447-497-1
11	18.4	61.3	485	3	US-09-533-559-2284
12	18	60.0	50	3	US-08-753-247-7
13	18	60.0	477	3	US-09-270-767-8822
14	18	60.0	477	3	US-09-270-767-24104
15	18	60.0	2142	3	US-08-753-247-8
16	17.8	59.3	601	3	US-09-949-016-44850
17	17.8	59.3	601	3	US-09-949-016-44851
18	17.8	59.3	601	3	US-09-949-016-73896
19	17.8	59.3	601	3	US-09-949-016-193773
20	17.8	59.3	601	3	US-09-949-002-4223
21	17.8	59.3	43690	3	US-09-949-016-13904
22	17.8	59.3	67745	3	US-09-949-016-17251
23	17.8	59.3	105189	3	US-09-949-016-13029
24	17.8	59.3	129554	3	US-09-949-002-765

25	17.8	59.3	179904	3	US-09-949-002-577	Sequence 577, App
26	17.8	59.3	179905	3	US-09-949-002-705	Sequence 705, App
27	17.6	58.7	3375	2	US-08-381-931B-1	Sequence 1, Appli
28	17.4	58.0	246	3	US-09-382-552-59	Sequence 59, Appli
29	17.4	58.0	705	3	US-08-781-420-8	Sequence 8, Appli
30	17.4	58.0	705	3	US-08-781-420-9	Sequence 9, Appli
31	17.4	58.0	705	3	US-08-874-102-9	Sequence 8, Appli
32	17.4	58.0	705	3	US-08-874-102-9	Sequence 9, Appli
33	17.4	58.0	705	3	US-08-984-919A-8	Sequence 8, Appli
34	17.4	58.0	705	3	US-08-984-919A-9	Sequence 9, Appli
35	17.4	58.0	705	3	US-09-006-595A-8	Sequence 8, Appli
36	17.4	58.0	705	3	US-09-006-595A-9	Sequence 9, Appli
37	17.4	58.0	707	3	US-08-781-420-5	Sequence 5, Appli
38	17.4	58.0	707	3	US-08-781-420-7	Sequence 7, Appli
39	17.4	58.0	707	3	US-08-874-102-5	Sequence 5, Appli
40	17.4	58.0	707	3	US-08-874-102-7	Sequence 7, Appli
41	17.4	58.0	707	3	US-08-984-919A-5	Sequence 5, Appli
42	17.4	58.0	707	3	US-08-984-919A-7	Sequence 7, Appli
43	17.4	58.0	707	3	US-09-006-595A-5	Sequence 5, Appli
44	17.4	58.0	707	3	US-09-006-595A-7	Sequence 7, Appli
45	17.4	58.0	993	3	US-09-489-039A-3737	Sequence 3737, Ap

ALIGNMENTS

RESULT 1

US-09-859-724-1

; Sequence 1, Application US/09859724

; Patent No. 6699843

; GENERAL INFORMATION:

; APPLICANT: Pietras, Kristian

; APPLICANT: Ostman, Arne

; APPLICANT: Heldin, Carl-Henrik

; APPLICANT: Rubin, Kristofer

; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING NUCLEIC ACID

; FILE REFERENCE: NEX90

; CURRENT APPLICATION NUMBER: US/09/859,724

; CURRENT FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/205,006

; PRIOR FILING DATE: 2000-05-17

; PRIOR APPLICATION NUMBER: 08/479,725

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/479,783

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/618,693

; PRIOR FILING DATE: 1996-03-20

; PRIOR APPLICATION NUMBER: 08/991,743

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Nucleic Acid Ligand

; NAME/KEY: modified base

; LOCATION: (6)..(30)

; OTHER INFORMATION: U at positions 6, 20 and 30 is

; OTHER INFORMATION: 2'-fluoro-2'-deoxyuridine

; NAME/KEY: modified base

; LOCATION: (8)..(29)

; OTHER INFORMATION: C at positions 8, 21, 28, and 29 is

; OTHER INFORMATION: 2'-fluoro-2'-deoxycytidine

; NAME/KEY: modified base

; LOCATION: (9)..(31)

; OTHER INFORMATION: G at positions 9, 15, 17, and 31 is

; OTHER INFORMATION: 2'-O-Methyl-2'-deoxyguanosine

; NAME/KEY: modified base

; LOCATION: (22)

; OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine
; NAME/KEY: modified base
; LOCATION: (1)..(30)
; OTHER INFORMATION: The residues at positions 9 and 10 are connected by a hexaethylen
; OTHER INFORMATION: phosphoramidite linker. The residues at positions 21 and 22 are
; OTHER INFORMATION: connected by a hexaethylene glycol phosphoramidite linker.
; NAME/KEY: modified_base
; LOCATION: (32)
; OTHER INFORMATION: Nucleotide 32 is an inverted orientation T
; OTHER INFORMATION: (3'-3'-linked)
US-09-859-724-1

Query Match 100.0%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
|||
Db 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30

RESULT 2

US-09-246-461-3
; Sequence 3, Application US/09246461
; Patent No. 6329145
; GENERAL INFORMATION:
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
; FILE REFERENCE: NEX78
; CURRENT APPLICATION NUMBER: US/09/246,461
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: ligand
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The t at position 1 is 2'-NH2. The u's and c's at
; OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
; OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
; OTHER INFORMATION: are 2'-O-methyl.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The g at position 10 and the a at position 22 have
; OTHER INFORMATION: been modified with polyethylene glycol of 18
; OTHER INFORMATION: units.
US-09-246-461-3

Query Match 100.0%; Score 30; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
|||
Db 2 CAGGCUACGCGTAGAGCAUCATGATCCUGT 31

RESULT 3

US-10-021-330-3
; Sequence 3, Application US/10021330
; Patent No. 6670132
; GENERAL INFORMATION:
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
; FILE REFERENCE: NEX78
; CURRENT APPLICATION NUMBER: US/09/246,461
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: ligand
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The t at position 1 is 2'-NH2. The u's and c's at
; OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
; OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
; OTHER INFORMATION: are 2'-O-methyl.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The g at position 10 and the a at position 22 have
; OTHER INFORMATION: been modified with polyethylene glycol of 18
; OTHER INFORMATION: units.
US-09-246-461-3

; FILE REFERENCE: NEX78
; CURRENT APPLICATION NUMBER: US/10/021,330
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/246,461
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: ligand
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The t at position 1 is 2'-NH2. The u's and c's at
; OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
; OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
; OTHER INFORMATION: are 2'-O-methyl.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(31)
; OTHER INFORMATION: The g at position 10 and the a at position 22 have
; OTHER INFORMATION: been modified with polyethylene glycol of 18
; OTHER INFORMATION: units.
US-10-021-330-3

Query Match 100.0%; Score 30; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
|||
Db 2 CAGGCUACGCGTAGAGCAUCATGATCCUGT 31

RESULT 4

US-09-270-767-11347
; Sequence 11347, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11347
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11347

Query Match 65.3%; Score 19.6; DB 3; Length 606;
Best Local Similarity 84.6%; Pred. No. 20;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATC 26
|||
Db 279 CAGGCGACGGGTGGAGCACCATGATC 304

RESULT 5

US-09-270-767-14489
; Sequence 14489, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14489
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-14489

Query Match 65.3%; Score 19.6; DB 3; Length 615;
Best Local Similarity 84.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATC 26
Db 117 CAGGCGACGGTGGAGCACCATGATC 142
||||| ||||| ||||| ||||| |||||

RESULT 6
US-09-270-767-10626
; Sequence 10626, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10626
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10626

Query Match 65.3%; Score 19.6; DB 3; Length 705;
Best Local Similarity 84.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCATGATC 26
Db 543 CAGGCGACGGTGGAGCACCATGATC 568
||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-949-016-16423
; Sequence 16423, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16423
; LENGTH: 167708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16423

Query Match 65.3%; Score 19.6; DB 3; Length 167708;
Best Local Similarity 73.1%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 5 CUACGCGTAGAGCAUCATGATCCUGT 30
Db 50558 CTACCGAGAGCATGCTGGTCTGT 50583
||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-489-039A-2715
; Sequence 2715, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2715
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2715

Query Match 63.3%; Score 19; DB 3; Length 603;
Best Local Similarity 74.1%; Pred. No. 39;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCUACGCGTAGAGCAUCATGATCCUG 29
Db 106 GGCACACGCTGGAGCATCATCTCTG 132
||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-447-497-4
; Sequence 4, Application US/09447497
; Patent No. 6773911
; GENERAL INFORMATION:
; APPLICANT: Penninger, Josef M.
; APPLICANT: Kroemer, Guido P.
; APPLICANT: Siderovski, David P.
; APPLICANT: Zamzami, Naoufal
; APPLICANT: Susin, Santos A.
; APPLICANT: Snow, Bryan E.L.
; TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR
; FILE REFERENCE: 01017/36780
; CURRENT APPLICATION NUMBER: US/09/447,497
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/109,595
; EARLIER FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1875)
; FEATURE:
; OTHER INFORMATION: mouse apoptosis-inducing factor (mAIF isoform);
; OTHER INFORMATION: mAIF-alt-exon-Gold
US-09-447-497-4

Query Match 62.7%; Score 18.8; DB 3; Length 1920;
Best Local Similarity 81.8%; Pred. No. 61;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 8 CCGGTAGAGCAUCATGATCCUG 29
Db 1387 CGAGTAGAGCATCATGATCATG 1408

RESULT 10
US-09-447-497-1
; Sequence 1, Application US/09447497
; Patent No. 6773911
; GENERAL INFORMATION:
; APPLICANT: Penninger, Josef M.
; APPLICANT: Kroemer, Guido P.
; APPLICANT: Siderovski, David P.
; APPLICANT: Zamzami, Naoufal
; APPLICANT: Susin, Santos A.
; APPLICANT: Snow, Bryan E.L.
; TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR
; FILE REFERENCE: 01017/36780
; CURRENT APPLICATION NUMBER: US/09/447,497
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/109,595
; EARLIER FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1887)
; FEATURE:
; OTHER INFORMATION: mouse apoptosis-inducing factor (mAIF);
; OTHER INFORMATION: mAIF-Gold.B1B
US-09-447-497-1

Query Match 62.7%; Score 18.8; DB 3; Length 1932;
Best Local Similarity 81.8%; Pred. No. 61;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCGGTAGAGCAUCATGATCCUG 29
Db 1399 CGAGTAGAGCATCATGATCATG 1420

RESULT 11
US-09-533-559-2284
; Sequence 2284, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2284
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(485)
; OTHER INFORMATION: n = A,T,C or G

US-09-533-559-2284
Query Match 61.3%; Score 18.4; DB 3; Length 485;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 20; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 AGGCUACGCGTAGAGCAUCATGATCCUG 29
Db 181 AGGCAGCGTTTGGGGCATCATGATCCTG 208

RESULT 12
US-08-753-247-7/c
; Sequence 7, Application US/08753247
; Patent No. 6210929
; GENERAL INFORMATION:
; APPLICANT: SCHLOKAT, Uwe
; APPLICANT: FISCHER, Bernhard
; APPLICANT: FALKNER, Falko-Guenther
; APPLICANT: DORNER, Friedrich
; APPLICANT: EIBL, Johann
; TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
; TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
; TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,247
; FILING DATE: 22-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AT 1928/95
; FILING DATE: 24-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40433/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-753-247-7

Query Match 60.0%; Score 18; DB 3; Length 50;
Best Local Similarity 69.2%; Pred. No. 68;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGCUACGCGTAGAGCAUCATGATCCU 28
Db 42 GGCCTGGCGGCGAGGCATCATCATCAT 17

RESULT 13
US-09-270-767-8822
; Sequence 8822, Application US/09270767
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```
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 822
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-822

Query Match      60.0%; Score 18; DB 3; Length 477;
Best Local Similarity 73.1%; Pred. No. 1.1e+02;
Matches 19; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 AGGUACGCGTAGAGCAUCATGATCC 27
      |||||:|||||:|||||:|||||:
DB      339 AGGCTATCGGTATAGCATGATTACC 364

RESULT 14
US-09-270-767-24104
; Sequence 24104, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24104
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-24104

Query Match      60.0%; Score 18; DB 3; Length 477;
Best Local Similarity 73.1%; Pred. No. 1.1e+02;
Matches 19; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 AGGUACGCGTAGAGCAUCATGATCC 27
      |||||:|||||:|||||:|||||:
DB      339 AGGCTATCGGTATAGCATGATTACC 364

RESULT 15
US-08-753-247-8
; Sequence 8, Application US/08753247
; Patent No. 6210929
; GENERAL INFORMATION:
; APPLICANT: SCHLOKAT, Uwe
; APPLICANT: FISCHER, Bernhard
; APPLICANT: FALKNER, Falko-Guenther
; APPLICANT: DORNER, Friedrich
; APPLICANT: EIBL, Johann
; TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
; TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
; TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,247
; FILING DATE: 22-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AT 1928/95
; FILING DATE: 24-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40433/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2139
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..2139
US-08-753-247-8

Query Match      60.0%; Score 18; DB 3; Length 2142;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 GGUACGCGTAGAGCAUCATGATCCU 28
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DB      2108 GGCTGCGCGCAGGGCATCATCATCAT 2133

Search completed: January 8, 2006, 17:08:34
Job time : 103 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 15:50:54 ; Search time 560 Seconds
(without alignments)
443.002 Million cell updates/sec

Title: US-10-791-367-1

Perfect score: 30

Sequence: 1 caggcuacgcgtagcaucgatcccgct 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_NA_Main:
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
 - 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
 - 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
 - 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
 - 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
 - 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
 - 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
 - 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
 - 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
 - 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	30	3	US-09-859-724-1
2	30	100.0	30	8	US-10-791-367-1
3	30	100.0	30	9	US-10-926-806-21
4	30	100.0	31	5	US-10-021-330-3
5	30	100.0	31	8	US-10-746-565-3
6	29	96.7	29	8	US-10-829-504A-8
7	29	96.7	29	9	US-10-873-853-8
8	29	96.7	29	9	US-10-980-211-8
9	19.8	66.0	2862	7	US-10-282-122A-41310
10	19.6	65.3	2349	10	US-11-097-143-16217
C 11	19.6	65.3	4992	10	US-11-097-143-16216
C 12	19.4	64.7	403	8	US-10-425-115-17734
13	19.4	64.7	1335	8	US-10-425-115-139288
14	19.2	64.0	466	7	US-10-767-701-23066
C 15	19	63.3	663	8	US-10-762-107-27
C 16	19	63.3	734	7	US-10-425-114-34193
C 17	19	63.3	734	8	US-10-425-115-145955
18	19	63.3	1359	7	US-10-437-963-24608
C 19	19	63.3	36602	8	US-10-762-107-1
C 20	19	63.3	2256646	7	US-10-470-565-1
21	18.8	62.7	396	7	US-10-424-599-92411
22	18.8	62.7	1617	8	US-10-481-113-4
23	18.8	62.7	1638	8	US-10-481-113-5

24	18.8	62.7	1857	7	US-10-437-963-74656	Sequence 74656, A
25	18.8	62.7	1920	6	US-10-308-936-4	Sequence 4, Appli
26	18.8	62.7	1932	6	US-10-308-936-1	Sequence 1, Appli
27	18.8	62.7	1932	7	US-10-419-256-1	Sequence 1, Appli
C 28	18.8	62.7	6899	3	US-09-938-842A-2030	Sequence 2030, Ap
C 29	18.8	62.7	6899	3	US-09-938-842A-2030	Sequence 2030, Ap
C 30	18.8	62.7	40633	5	US-10-087-132-1	Sequence 1, Appli
C 31	18.6	62.0	573	7	US-10-021-323-3107	Sequence 3107, Ap
C 32	18.6	62.0	652	7	US-10-021-323-1390	Sequence 1390, Ap
C 33	18.6	62.0	1430	8	US-10-767-795-86	Sequence 86, Appl
34	18.6	62.0	1944	7	US-10-437-963-31340	Sequence 31340, A
C 35	18.6	62.0	12195	9	US-10-661-398-13	Sequence 13, Appl
C 36	18.6	62.0	16061	9	US-10-661-398-12	Sequence 12, Appl
C 37	18.4	61.3	147	8	US-10-425-115-150217	Sequence 150217,
38	18.4	61.3	353	3	US-09-922-293-2640	Sequence 2640, Ap
39	18.4	61.3	485	8	US-10-653-047-2284	Sequence 2284, Ap
C 40	18.4	61.3	602	4	US-09-925-065A-422787	Sequence 422787,
41	18.4	61.3	646	5	US-10-027-632-319063	Sequence 319063,
42	18.4	61.3	646	6	US-10-027-632-319063	Sequence 319063,
C 43	18	60.0	541	4	US-09-925-065A-662266	Sequence 662266,
C 44	18	60.0	602	4	US-09-925-065A-788924	Sequence 788924,
C 45	18	60.0	602	4	US-09-925-065A-847051	Sequence 847051,

ALIGNMENTS

RESULT 1

- US-09-859-724-1
- ; Sequence 1, Application US/09859724
 - ; Patent No. US20020034506A1
 - ; GENERAL INFORMATION:
 - ; APPLICANT: Pietras, Kristian
 - ; APPLICANT: Ostman, Arne
 - ; APPLICANT: Helgin, Carl-Henrik
 - ; APPLICANT: Rubin, Kristofer
 - ; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING NUCLEIC ACID
 - ; FILE REFERENCE: NEX90
 - ; FILE REFERENCE: LIGANDS TO PDGF
 - ; CURRENT APPLICATION NUMBER: US/09/859,724
 - ; CURRENT FILING DATE: 2001-09-21
 - ; PRIOR APPLICATION NUMBER: 60/205,006
 - ; PRIOR FILING DATE: 2000-05-17
 - ; PRIOR APPLICATION NUMBER: 08/479,725
 - ; PRIOR FILING DATE: 1995-06-07
 - ; PRIOR APPLICATION NUMBER: 08/479,783
 - ; PRIOR FILING DATE: 1995-06-07
 - ; PRIOR APPLICATION NUMBER: 08/618,693
 - ; PRIOR FILING DATE: 1996-03-20
 - ; PRIOR APPLICATION NUMBER: 08/991,743
 - ; PRIOR FILING DATE: 1997-12-16
 - ; NUMBER OF SEQ ID NOS: 2
 - ; SOFTWARE: PatentIn Ver. 2.0
 - ; SEQ ID NO 1
 - ; LENGTH: 30
 - ; TYPE: DNA
 - ; ORGANISM: Artificial Sequence
 - ; FEATURE:
 - ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 - ; OTHER INFORMATION: Nucleic Acid Ligand
 - ; NAME/KEY: modified base
 - ; LOCATION: (6)..(30)
 - ; OTHER INFORMATION: U at positions 6, 20 and 30 is
 - ; OTHER INFORMATION: 2'-fluoro-2'-deoxyuridine
 - ; NAME/KEY: modified base
 - ; LOCATION: (8)..(29)
 - ; OTHER INFORMATION: C at positions 8, 21, 28, and 29 is
 - ; OTHER INFORMATION: 2'-fluoro-2'-deoxycytidine
 - ; NAME/KEY: modified base
 - ; LOCATION: (9)..(31)
 - ; OTHER INFORMATION: G at positions 9, 15, 17, and 31 is
 - ; OTHER INFORMATION: 2'-O-Methyl-2'-deoxyguanosine
 - ; NAME/KEY: modified base

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/ LOCATION: (22)
/ OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine
/ NAME/KEY: modified_base
/ LOCATION: (1)..(30)
/ OTHER INFORMATION: The residues at positions 9 and 10 are connected by a hexaethylene
/ OTHER INFORMATION: phosphoramidite linker. The residues at positions 21 and 22 are
/ NAME/KEY: modified_base
/ LOCATION: (32)
/ OTHER INFORMATION: Nucleotide 32 is an inverted orientation T
/ OTHER INFORMATION: (3'-3'-linked)
US-09-859-724-1

Query Match      100.0%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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Db 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30

RESULT 2
US-10-791-367-1
/ Sequence 1, Application US/10791367
/ Publication No. US20040224335A1
/ GENERAL INFORMATION:
/ APPLICANT: Pietras, Kristian
/ APPLICANT: Ostman, Arne
/ APPLICANT: Heldin, Carl-Henrik
/ APPLICANT: Rubin, Kristofer
/ TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING NUCLEIC ACID
/ TITLE OF INVENTION: LIGANDS TO PDGF
/ FILE REFERENCE: NEX90
/ CURRENT APPLICATION NUMBER: US/10/791,367
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/859,724
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/205,006
/ PRIOR FILING DATE: 2000-05-17
/ PRIOR APPLICATION NUMBER: 08/479,725
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/479,783
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/618,693
/ PRIOR FILING DATE: 1996-03-20
/ PRIOR APPLICATION NUMBER: 08/991,743
/ PRIOR FILING DATE: 1997-12-16
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Nucleic Acid Ligand
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (6)..(30)
/ OTHER INFORMATION: U at positions 6, 20 and 30 is
/ OTHER INFORMATION: 2'-fluoro-2'-deoxyuridine
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (8)..(29)
/ OTHER INFORMATION: C at positions 8, 21, 28, and 29 is
/ OTHER INFORMATION: 2'-fluoro-2'-deoxycytidine
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (9)..(31)
/ OTHER INFORMATION: G at positions 9, 15, 17, and 31 is
/ OTHER INFORMATION: 2'-O-Methyl-2'-deoxyguanosine
/ FEATURE:
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/ NAME/KEY: modified_base
/ LOCATION: (22)
/ OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (1)..(30)
/ OTHER INFORMATION: The residues at positions 9 and 10 are connected by a hexaethylene
/ OTHER INFORMATION: phosphoramidite linker. The residues at positions 21 and 22 are
/ NAME/KEY: modified_base
/ LOCATION: (32)
/ OTHER INFORMATION: Nucleotide 32 is an inverted orientation T
/ OTHER INFORMATION: (3'-3'-linked)
US-10-791-367-1

Query Match      100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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Db 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30

RESULT 3
US-10-926-806-21
/ Sequence 21, Application US/10926806
/ Publication No. US2005009257A1
/ GENERAL INFORMATION:
/ APPLICANT: SHIMA, DAVID
/ APPLICANT: CALIAS, PERRY
/ APPLICANT: ADAMIS, ANTHONY P.
/ TITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
/ TITLE OF INVENTION: NEOVASCULAR DISORDERS
/ FILE REFERENCE: 112089.184 EYE-013
/ CURRENT APPLICATION NUMBER: US/10/926,806
/ CURRENT FILING DATE: 2004-08-26
/ PRIOR APPLICATION NUMBER: 60/556,837
/ PRIOR FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER: 60/498,407
/ PRIOR FILING DATE: 2003-08-27
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 21
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: anti-PDGF aptamer
US-10-926-806-21

Query Match      100.0%; Score 30; DB 9; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.00046;
Matches 27; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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Db 1 CAGGCTACGCGTAGAGCATCATGATCCTGT 30

RESULT 4
US-10-021-330-3
/ Sequence 3, Application US/10021330
/ Publication No. US20020197617A1
/ GENERAL INFORMATION:
/ APPLICANT: Janjic, Nebojsa
/ APPLICANT: Gold, Larry
/ TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
/ FILE REFERENCE: NEX78
/ CURRENT APPLICATION NUMBER: US/10/021,330
/ CURRENT FILING DATE: 2001-12-10
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;; PRIOR APPLICATION NUMBER: US/09/246,461
;; PRIOR FILING DATE: 1999-02-09
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
;; OTHER INFORMATION: ligand
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (1)..(31)
;; OTHER INFORMATION: The t at position 1 is 2'-NH₂. The u's and c's at
;; OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
;; OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
;; OTHER INFORMATION: are 2'-O-methyl.
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (1)..(31)
;; OTHER INFORMATION: The g at position 10 and the a at position 22 have
;; OTHER INFORMATION: been modified with polyethylene glycol of 18
;; OTHER INFORMATION: units.
US-10-021-330-3

Query Match 100.0%; Score 30; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCAUGATGATCCUGT 30
Db 2 CAGGCUACGCGTAGAGCAUCAUGATGATCCUGT 31

RESULT 5
US-10-746-565-3
;; Sequence 3, Application US/10746565
;; Publication No. US20050048521A1
;; GENERAL INFORMATION:
;; APPLICANT: Janjic, Nebojsa
;; APPLICANT: Gold, Larry
;; TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
;; FILE REFERENCE: NEX78
;; CURRENT APPLICATION NUMBER: US/10/746,565
;; CURRENT FILING DATE: 2003-12-24
;; PRIOR APPLICATION NUMBER: US/10/021,330
;; PRIOR FILING DATE: 2001-12-10
;; PRIOR APPLICATION NUMBER: US/09/246,461
;; PRIOR FILING DATE: 1999-02-09
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
;; OTHER INFORMATION: ligand
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (1)..(31)
;; OTHER INFORMATION: The t at position 1 is 2'-NH₂. The u's and c's at
;; OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
;; OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
;; OTHER INFORMATION: are 2'-O-methyl.
;; FEATURE:
;; NAME/KEY: modified base
;; LOCATION: (1)..(31)
;; OTHER INFORMATION: The g at position 10 and the a at position 22 have
;; OTHER INFORMATION: been modified with polyethylene glycol of 18
;; OTHER INFORMATION: units.
US-10-746-565-3

Query Match 100.0%; Score 30; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCAUGATGATCCUGT 30
Db 2 CAGGCUACGCGTAGAGCAUCAUGATGATCCUGT 31

RESULT 6
US-10-829-504A-8
;; Sequence 8, Application US/10829504A
;; Publication No. US20040253679A1
;; GENERAL INFORMATION:
;; APPLICANT: Epstein, David
;; APPLICANT: Grate, Dilara
;; APPLICANT: Stanton, Martin
;; APPLICANT: Diener, John L.
;; APPLICANT: Wilson, Charles
;; APPLICANT: McCauley, Thomas
;; APPLICANT: DeSouza, Errol
;; TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and Their
;; TITLE OF INVENTION: Use as Oncology Therapeutics
;; FILE REFERENCE: 23239-558A
;; CURRENT APPLICATION NUMBER: US/10/829,504A
;; CURRENT FILING DATE: 2004-04-21
;; PRIOR APPLICATION NUMBER: 10/762915
;; PRIOR FILING DATE: 2004-01-21
;; PRIOR APPLICATION NUMBER: 60/441357
;; PRIOR FILING DATE: 2003-01-21
;; PRIOR APPLICATION NUMBER: 60/463095
;; PRIOR FILING DATE: 2003-04-15
;; PRIOR APPLICATION NUMBER: 60/464179
;; PRIOR FILING DATE: 2003-04-21
;; PRIOR APPLICATION NUMBER: 60/465055
;; PRIOR FILING DATE: 2003-04-23
;; PRIOR APPLICATION NUMBER: 60/469628
;; PRIOR FILING DATE: 2003-05-08
;; PRIOR APPLICATION NUMBER: 60/474680
;; PRIOR FILING DATE: 2003-05-29
;; PRIOR APPLICATION NUMBER: 60/491019
;; PRIOR FILING DATE: 2003-07-29
;; PRIOR APPLICATION NUMBER: 60/512071
;; PRIOR FILING DATE: 2003-10-17
;; PRIOR APPLICATION NUMBER: 60/537201
;; PRIOR FILING DATE: 2004-01-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 98
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 8
;; LENGTH: 29
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: aptamer
US-10-829-504A-8

Query Match 96.7%; Score 29; DB 8; Length 29;
Best Local Similarity 89.7%; Pred. No. 0.0014;
Matches 26; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGCUACGCGTAGAGCAUCAUGATGATCCUG 29
Db 1 CAGGCUACGCGTAGAGCAUCAUGATGATCCUG 29

RESULT 7
US-10-873-853-8
;; Sequence 8, Application US/10873853
;; Publication No. US20050124565A1
;; GENERAL INFORMATION:
;; APPLICANT: Epstein, David


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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41310
; LENGTH: 2862
; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-282-122A-41310

Query Match
Best Local Similarity 66.0%; Score 19.8; DB 7; Length 2862;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGCGTAGAGCAUCATGATCCUG 29
||||| ||||| ||||| ||||| |||||
Db 98 AGCGTAGAGCAUCATGATCCG 120

RESULT 10
US-11-097-143-16217
; Sequence 16217, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16217
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-16217

Query Match
Best Local Similarity 65.3%; Score 19.6; DB 10; Length 2349;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATC 26
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Db 1851 CAGGCGACGGTGGAGCACCACATGATC 1876

RESULT 11
US-11-097-143-16216/c
; Sequence 16216, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16217
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-16217

Query Match
Best Local Similarity 65.3%; Score 19.6; DB 10; Length 2349;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATC 26
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Db 1851 CAGGCGACGGTGGAGCACCACATGATC 1876

RESULT 12
US-10-425-115-17734/c
; Sequence 17734, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 17734
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116177C.1
US-10-425-115-17734

Query Match
Best Local Similarity 64.7%; Score 19.4; DB 8; Length 403;
Matches 20; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 AGGCUACGCGTAGAGCAUCATGATCCUCT 30
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Db 330 AGCCTCCGCGTAGTGGATCAAGATGCTGT 302

RESULT 13
US-10-425-115-139288
; Sequence 139288, Application US/10425115
; Publication No. US20040214272A1
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 15:55:54 ; Search time 243 Seconds
(without alignments)
89.992 Million cell updates/sec

Title: US-10-791-367-1

Perfect score: 30

Sequence: 1 caggcuacgcgtagcaucgatccct 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4637609 seqs, 36448668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.New.*

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	18.4	61.3	151169	7	US-11-121-086-38	Sequence 38, Appl
C 2	17.8	59.3	1110	6	US-10-750-185-25891	Sequence 25891, A
C 3	17.8	59.3	1110	6	US-10-750-623-25891	Sequence 25891, A
C 4	17.8	59.3	146656	7	US-11-121-086-68	Sequence 68, Appl
C 5	17.4	58.0	762	6	US-10-750-185-53338	Sequence 53338, A
C 6	17.4	58.0	762	6	US-10-750-623-53338	Sequence 53338, A
C 7	17.4	58.0	1002	7	US-11-127-877-20	Sequence 20, Appl
C 8	17.4	58.0	1733	6	US-10-750-185-26283	Sequence 26283, A
C 9	17.4	58.0	1733	6	US-10-750-623-26283	Sequence 26283, A
C 10	17.2	57.3	1400	7	US-11-136-527-4382	Sequence 4382, App
C 11	17.2	57.3	1696	7	US-11-136-527-4382	Sequence 4382, App
C 12	17.2	57.3	4347	7	US-11-136-527-286	Sequence 286, App
C 13	17	56.7	201	6	US-10-995-561-11799	Sequence 11799, A
C 14	17	56.7	201	6	US-10-995-561-11837	Sequence 11837, A
C 15	17	56.7	201	6	US-10-995-561-61360	Sequence 61360, A
C 16	17	56.7	4947	6	US-10-995-561-457	Sequence 457, App
C 17	17	56.7	5130	7	US-11-135-855-12	Sequence 12, Appl
C 18	17	56.7	5158	7	US-11-135-855-13	Sequence 13, Appl
C 19	17	56.7	6719	6	US-10-995-561-456	Sequence 456, App
C 20	17	56.7	32157	6	US-10-995-561-13352	Sequence 13352, A
C 21	16.8	56.0	189	7	US-11-108-172-103	Sequence 103, App
C 22	16.8	56.0	261	7	US-11-108-172-749	Sequence 749, App
C 23	16.8	56.0	387	6	US-10-467-657-2599	Sequence 2599, Ap

ALIGNMENTS

RESULT 1

US-11-121-086-38/c
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-38

Query Match 61.3%; Score 18.4; DB 7; Length 151169;
Best Local Similarity 67.9%; Pred. No. 73;
Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGGCUACGCCTAGCAUCAUCATGATCCU 28
DB 46374 CAGGATAGGAATATAGCTTCATGATCCT 46347

RESULT 2

US-10-750-185-25891
; Sequence 25891, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

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; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25891
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Bovine 19866881126825
US-10-750-185-25891

Query Match      59.3%; Score 17.8; DB 6; Length 1110;
Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AGGCUACGGGTAGAGCAUCATGATCCUGT 30
Db 595 AGGTACACATTCAGCATACTGATCCTGT 623

RESULT 4
US-10-750-623-25891
; Sequence 25891, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25891
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Bovine 19866881126825
US-10-750-623-25891

Query Match      59.3%; Score 17.8; DB 6; Length 1110;
Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AGGCUACGGGTAGAGCAUCATGATCCUGT 30
Db 595 AGGTACACATTCAGCATACTGATCCTGT 623

RESULT 4
US-11-121-086-68/c
; Sequence 68, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 146656
; TYPE: DNA
; ORGANISM: Homo sapiens

; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25891
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Bovine 19866881126825
US-10-750-185-25891

Query Match      59.3%; Score 17.8; DB 6; Length 1110;
Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AGGCUACGGGTAGAGCAUCATGATCCUGT 30
Db 595 AGGTACACATTCAGCATACTGATCCTGT 623

RESULT 4
US-10-750-623-25891
; Sequence 25891, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25891
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Bovine 19866881126825
US-10-750-623-25891

Query Match      59.3%; Score 17.8; DB 6; Length 1110;
Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AGGCUACGGGTAGAGCAUCATGATCCUGT 30
Db 595 AGGTACACATTCAGCATACTGATCCTGT 623

RESULT 4
US-11-121-086-68/c
; Sequence 68, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 146656
; TYPE: DNA
; ORGANISM: Homo sapiens

; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25891
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Bovine 19866881126825
US-10-750-185-25891

Query Match      59.3%; Score 17.8; DB 6; Length 1110;
Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AGGCUACGGGTAGAGCAUCATGATCCUGT 30
Db 595 AGGTACACATTCAGCATACTGATCCTGT 623

RESULT 4
US-10-750-623-25891
; Sequence 25891, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53338
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Bovine 19866881728240
US-10-750-185-53338

Query Match      58.0%; Score 17.4; DB 6; Length 762;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGCUACGGGTAGAGCAUCATGATCCUG 29
Db 123 GGCTACTCGGAGTGCATCGTGACCGTG 97

RESULT 6
US-10-750-623-53338/c
; Sequence 53338, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53338
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Bovine 19866881728240
US-10-750-623-53338

Query Match      58.0%; Score 17.4; DB 6; Length 762;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGCUACGGGTAGAGCAUCATGATCCUG 29
Db 123 GGCTACTCGGAGTGCATCGTGACCGTG 97

RESULT 6
US-10-750-623-53338/c
; Sequence 53338, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53338
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Bovine 19866881728240
US-10-750-623-53338

Query Match      58.0%; Score 17.4; DB 6; Length 762;
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Best Local Similarity 66.7%; Pred. No. 94;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 GCUACGGCTAGAGCAUCATGATCCUG 29
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Db 123 GCGTACTCGGAGTGCATCGTGACCGTG 97

RESULT 7
US-11-127-877-20
; Sequence 20, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-20

Query Match 58.0%; Score 17.4; DB 7; Length 1002;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GCUACGGCTAGAGCAUCATGATCCUGT 30
   |||:|||||:|||||:|||||:|
Db 611 GCTAGTGGAGATCTTCAGACCTGT 637

RESULT 8
US-10-750-185-26283
; Sequence 26283, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26283
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Bovine 19866881128530
US-10-750-185-26283

Query Match 58.0%; Score 17.4; DB 6; Length 1733;
Best Local Similarity 70.4%; Pred. No. 1.1e+02;
Matches 19; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 GCUACGGCTAGAGCAUCATGATCCUGT 30
   |||:|||||:|||||:|||||:|
Db 1042 GTTACACCAAGCAGCAGCATGATCCTTT 1068

RESULT 9
US-10-750-623-26283
; Sequence 26283, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26283
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Bovine 19866881128530
US-10-750-623-26283

Query Match 58.0%; Score 17.4; DB 6; Length 1733;
Best Local Similarity 70.4%; Pred. No. 1.1e+02;
Matches 19; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 GCUACGGCTAGAGCAUCATGATCCUGT 30
   |||:|||||:|||||:|||||:|
Db 1042 GTTACACCAAGCAGCAGCATGATCCTTT 1068

RESULT 10
US-11-136-527-4382/c
; Sequence 4382, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4382
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4382

Query Match 57.3%; Score 17.2; DB 7; Length 1400;
Best Local Similarity 63.3%; Pred. No. 1.3e+02;
Matches 19; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CAGCUACGGCTAGAGCAUCATGATCCUGT 30
   |||:|||||:|||||:|||||:|
Db 511 CAGCATCGTGTAGGGCATCTGGCTCCTGT 482

RESULT 11
US-11-136-527-224/c
; Sequence 224, Application US/11136527
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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 224
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-224

Query Match      57.3%; Score 17.2; DB 7; Length 1696;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CAGGCUACCGGTAGAGCAUCATGATCCUGT 30
    |||||:|||||:|||||:|||||:|||||
Db 1063 CAGCCTCCGTGTAGGCGATCTTCATTCGGT 1034

RESULT 12
US-11-136-527-286/c
; Sequence 286, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 286
; LENGTH: 4347
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-286

Query Match      57.3%; Score 17.2; DB 7; Length 4347;
Best Local Similarity 63.3%; Pred. No. 1.5e+02;
Matches 19; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CAGGCUACCGGTAGAGCAUCATGATCCUGT 30
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Db 3458 CAGCATCCGTGTAGGCGATCTGGCTCCTGT 3429

RESULT 13
US-10-995-561-11799/c
; Sequence 11799, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11799
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-11799

Query Match      56.7%; Score 17; DB 6; Length 201;
Best Local Similarity 72.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGGCUACCGGTAGAGCAUCATGAT 25
    |||||:|||||:|||||:|||||:|||||
Db 179 CAGGCTCCACGAGACCATCATGTT 155

RESULT 14
US-10-995-561-11837/c
; Sequence 11837, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11837
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-11837

Query Match      56.7%; Score 17; DB 6; Length 201;
Best Local Similarity 72.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGGCUACCGGTAGAGCAUCATGAT 25
    |||||:|||||:|||||:|||||:|||||
Db 179 CAGGCTCCACGAGACCATCATGTT 155

RESULT 15
US-10-995-561-61360/c
; Sequence 61360, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61360
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-61360

Query Match      56.7%; Score 17; DB 6; Length 201;
Best Local Similarity 72.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGGCUACCGGTAGAGCAUCATGAT 25
    |||||:|||||:|||||:|||||:|||||
Db 179 CAGGCTCCACGAGACCATCATGTT 155

Search completed: January 8, 2006, 17:22:16
Job time : 245 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 15:02:49 ; Search time 1726 Seconds
(without alignments)
988.009 Million cell updates/sec

Title: US-10-791-367-1

Perfect score: 30

Sequence: 1 caggcuacgcgtagcaucaatgatccugt 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	30	6	CS079386	Sequence
2	30	100.0	30	6	AR481874	Sequence
3	30	100.0	31	6	BD249885	Aptamers
4	30	100.0	31	6	AR366193	Sequence
5	30	100.0	31	6	AR442638	Sequence
C 6	21.6	72.0	214332	14	AC120945	AC120945 Rattus no
7	21	70.0	226789	14	AC123112	AC123112 Rattus no
8	20	66.7	6002	15	AJ616913	AJ616913 Sordaria
9	20	66.7	110000	1	BS571965.10	Continuation (11 o
C 10	20	66.7	110000	1	CP000010_23	Continuation (24 o
11	20	66.7	163878	2	AC150398	AC150398 Branchios
C 12	20	66.7	172391	14	AC155516	AC155516 Zea mays
13	20	66.7	174912	14	AC145730	AC145730 Zea mays
C 14	20	66.7	181826	14	AC155574	AC155574 Zea mays
15	19.8	66.0	10205	1	AE004320	AE004320 Vibrio ch
16	19.6	65.3	606	6	AR506387	Sequence
17	19.6	65.3	615	6	AR509529	Sequence
18	19.6	65.3	705	6	AR505666	Sequence

19	19.6	65.3	2186	2	AY058696	AY058696 Drosophil
20	19.6	65.3	2349	6	CQ588459	Sequence
21	19.6	65.3	2782	2	AY052083	Drosophil
C 22	19.6	65.3	4992	6	CQ588458	Sequence
23	19.6	65.3	49054	14	AC019890	AC019890 Drosophil
24	19.6	65.3	104135	8	AC113373	AC113373 Homo sapi
C 25	19.6	65.3	123275	8	AC008779	AC008779 Homo sapi
26	19.6	65.3	175867	2	AC007976	AC007976 Drosophil
C 27	19.6	65.3	185689	13	AY261364	AY261364 African B
28	19.6	65.3	346734	2	AE003584	AE003584 Drosophil
29	19.4	64.7	153129	9	AC163209	AC163209 Mus muscu
C 30	19.4	64.7	169815	9	AC122057	AC122057 Mus muscu
31	19.4	64.7	175651	14	AC150605	AC150605 Callithri
C 32	19.4	64.7	230041	9	AC111047	AC111047 Mus muscu
33	19.4	64.7	251257	14	AC095972	AC095972 Rattus no
34	19.2	64.0	159866	8	AC016598	AC016598 Homo sapi
35	19	63.3	603	6	AR385986	AR385986 Sequence
C 36	19	63.3	663	6	CQ879025	Sequence
37	19	63.3	1269	6	AX653992	Sequence
C 38	19	63.3	1692	9	BC085826	Rattus no
C 39	19	63.3	36602	6	CQ878999	Sequence
C 40	19	63.3	44343	1	AP004312	AP004312 Synchocy
C 41	19	63.3	87792	15	AP003837	AP003837 Oryza sat
42	19	63.3	110000	1	AE014295.21	Continuation (22 o
C 43	19	63.3	110000	15	AP006213_058	Continuation (59 o
44	19	63.3	114104	9	BX545849	BX545849 Mouse DNA
C 45	19	63.3	151721	15	AP003943	AP003943 Oryza sat

ALIGNMENTS

RESULT 1	CS079386	Sequence 21 from Patent WO2005020972.	30 bp	DNA	linear	PAT 06-MAY-2005
LOCUS	CS079386					
DEFINITION	CS079386					
ACCESSION	CS079386.1	GI:63093789				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Qy						
Db						
RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						

ACCESSION	AC123112	unordered pieces.	COMMENT	On May 13, 2003 this sequence version replaced gi:23265213. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
VERSION	AC123112.4	GI:30598864		
KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Rattus.			
AUTHORS	Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, P., Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hawes, A., Henderson, N., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hladun, S. L., Hodgson, A., Hogue, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulsegged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangun, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarnpunaagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Stealm, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.			
TITLE	Direct Submission			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 226789)			
AUTHORS	Worley, K. C.			
TITLE	Direct Submission			
JOURNAL	Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
REFERENCE	3 (bases 1 to 226789)			
AUTHORS	Rat Genome Sequencing Consortium.			
TITLE	Direct Submission			
JOURNAL	Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
FEATURES	source	1. 226789		
misc_feature	misc_feature	1. 1460		
gap	gap	225475..225574		
ORIGIN	Query Match	70.0%; Score 21; DB 14; Length 226789;		
	Best Local Similarity	72.4%; Pred. No. 1.9e+02;		
	Matches	21; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		
	QY	1 CAGGCUACGCGTAGAGCAUCATGATCCUG 29		
	Db	187544 CAGGATACCTTAGAGCATCAGCATCTG 187572		
RESULT 8				
AJ616913				
LOCUS				
DEFINITION	Sordaria macrospora pro40 gene for putative signalling cascade			

component, exons 1-2.
AJ616913
VERSION AJ616913.1 GI:39645990
KEYWORDS pro40 gene; putative signalling cascade component.
SOURCE Sordaria macrospora
ORGANISM Sordaria macrospora
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
1
REFERENCE
AUTHORS Witzel-Schloemp,K., Strauch,P., Zhang,H. and Kueck,U.
TITLE Molecular genetic characterization of the developmental mutant pro40 from Sordaria macrospora: Identification of a putative component of a signalling cascade
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6002)
AUTHORS Witzel-Schloemp,K.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-2003) Witzel-Schloemp K., LS Allgemeine und Molekulare Botanik, Ruhr-Universitaet Bochum, Universitaetstrasse 150, 44780 Bochum, GERMANY
FEATURES
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/protein_id="CA883713.1"
/db_xref="GI:39645991"
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SPTEKPGADRRGAVPKLQSPDSPGTGDDLFAKPLGRPVQOQAQQAQHPAORISN
AYQOQYYPGGGVNKRSESIARISSTASTSTTRASRGSPPPTPIPEPVGIVG
GGEARYAAGISGTATLTSQAANAKLAQYGGORPPSPKPHKQHPALAAQS
QOQOQAQPPRPPTPTSPDQPGFPTVYQGDVAQNPAPQPQQNSYNLFPK
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APPLPEGTHLDQSGQYIIHLATQATQWEFFPKGFNFSHEAAELSPSTASYGNR
LASPLGKAGLASPMHPQTPGVAESIMTVAASPGFTGPPSPASQVMKYIMPTNG
VYFGLRYLNMDELKGIWHGSIIMVTDAQPPTTHLSVDLSPNQRQIPIHNIMTH
QRWVFYKMDLQMSBHGTERWTYAVTSHLGCTRYEFIVAGRYETGWRMLTAHSCNDFP
PSTVONERAKLGGVGMFKDILQNVCEGGFHVQLGDOIYGRDLREWPEPLLKQWLS
IAGRENKNVPTARHEEDVTHAEVHYTSHFDQPFMREAFQIPIVLIQDDHIDPDG
FGSPYEWQSSALPKNIGRIADIMYLLFQSHTTVEMLRNSSMDLFTTCAGWHFVIT
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ETVELTANTATGKKAVNSTYLLNGKVTSSVAGVVGKGVVAGHKEVTRAVGKSGML
GVNLQGFEDIAEELKDLMTWHSKOLERTYLIRTLQIGIAAQGVRMTFLSGDVSSAG
AGLLHDPSPSHDKTWQVLTISPIVAAPCSSYLLKALHSGSNKKLTVPLNGHKSHTH
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GGVAASVHSGSGSGGGLGNKLISLAVDFVVGQDGAFTATTIKYIGPVIIPHLEYGH"

exon 348..3768
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/number=1
variation 3060
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/notes="premature stop codon which causes defects in fruiting body maturation"
/evidence=experimental
/replacement=""
3769..3830
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intron 3831..4360
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exon

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ORIGIN
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Query Match          66.7%; Score 20; DB 15; Length 6002;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 20; Conservative 3; Mismatches 5; Indels 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCU 28
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Db 2284 CAGGCTACGCGGAAAGCATCATGACCGT 2311

RESULT 9
BX571965_10
WPCOMMENT
Sequence split into 41 fragments LOCUS BX571965 Accession BX571965
Fragment Name      Begin      End
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BX571965_02      300001  4100000
BX571965_03      400001  5100000
BX571965_04      500001  6100000
BX571965_05      600001  7100000
BX571965_06      700001  8100000
BX571965_07      800001  9100000
BX571965_08      900001  1010000
BX571965_09      1000001 1110000
BX571965_10      1100001 1210000
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BX571965_12      1300001 1410000
BX571965_13      1400001 1510000
BX571965_14      1500001 1610000
BX571965_15      1600001 1710000
BX571965_16      1700001 1810000
BX571965_17      1800001 1910000
BX571965_18      1900001 2010000
BX571965_19      2000001 2110000
BX571965_20      2100001 2210000
BX571965_21      2200001 2310000
BX571965_22      2300001 2410000
BX571965_23      2400001 2510000
BX571965_24      2500001 2610000
BX571965_25      2600001 2710000
BX571965_26      2700001 2810000
BX571965_27      2800001 2910000
BX571965_28      2900001 3010000
BX571965_29      3000001 3110000
BX571965_30      3100001 3210000
BX571965_31      3200001 3310000
BX571965_32      3300001 3410000
BX571965_33      3400001 3510000
BX571965_34      3500001 3610000
BX571965_35      3600001 3710000
BX571965_36      3700001 3810000
BX571965_37      3800001 3910000
BX571965_38      3900001 4010000
BX571965_39      4000001 4074542
BX571965_40      4000001 4074542
Continuation (11 of 41) of BX571965 from base 1000001 (BX571965 Burkha

Query Match          66.7%; Score 20; DB 1; Length 110000;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 21; Conservative 2; Mismatches 5; Indels 0;

QY 3 GGCUACGCGTAGAGCAUCATGATCCUGT 30
    |||||:|||||:|||||:|||||:
Db 53276 GGCTACGCGTAGAGCTCGTGATCCTGT 53303

RESULT 10
CP000010_23/c
WPCOMMENT
Sequence split into 36 fragments LOCUS CP000010 Accession CP000010

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Fragment Name      Begin      End
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CP000010_01      100001  210000
CP000010_02      200001  310000
CP000010_03      300001  410000
CP000010_04      400001  510000
CP000010_05      500001  610000
CP000010_06      600001  710000
CP000010_07      700001  810000
CP000010_08      800001  910000
CP000010_09      900001  1010000
CP000010_10     1000001 1110000
CP000010_11     1100001 1210000
CP000010_12     1200001 1310000
CP000010_13     1300001 1410000
CP000010_14     1400001 1510000
CP000010_15     1500001 1610000
CP000010_16     1600001 1710000
CP000010_17     1700001 1810000
CP000010_18     1800001 1910000
CP000010_19     1900001 2010000
CP000010_20     2000001 2110000
CP000010_21     2100001 2210000
CP000010_22     2200001 2310000
CP000010_23     2300001 2410000
CP000010_24     2400001 2510000
CP000010_25     2500001 2610000
CP000010_26     2600001 2710000
CP000010_27     2700001 2810000
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CP000010_33     3300001 3410000
CP000010_34     3400001 3510000
CP000010_35     3500001 3510148
Continuation (24 of 36) of CP000010 from base 2300001 (CP000010 Burkholderia mallei ATCC

Query Match      66.7%; Score 20; DB 1; Length 110000;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  3  GGCUACGCGTAGAGCAUCATGATCCUGT 30
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Db   32065  GGCACGCGTAGACGCTCGCTGATCCTGT 32038

RESULT 11
AC150398
LOCUS      AC150398      163878 bp      DNA      linear      INV 12-NOV-2004
DEFINITION Branchiostoma floridae clone CH302-18L14, complete sequence.
ACCESSION  AC150398
VERSION     AC150398.3 GI:55701323
KEYWORDS   HTG.
SOURCE     Branchiostoma floridae (Florida lancelet)
ORGANISM   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Quackenbush, J.
REFERENCE  1 (bases 1 to 163878)
AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE     Direct Submission
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 163878)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUL-2004) Production Genomics Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
            94598-1698, USA
REFERENCE  3 (bases 1 to 163878)
AUTHORS   Stanford Human Genome Center.
CONSRMTM  DOE Joint Genome Institute
TITLE     Direct Submission

```

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JOURNAL          Submitted (28-OCT-2004) DOE Joint Genome Institute, 2800 Mitchell
REFERENCE        4 (bases 1 to 163878)
AUTHORS          Stanford Human Genome Center.
CONSRMTM         DOE Joint Genome Institute
TITLE            Direct Submission
JOURNAL          Submitted (12-NOV-2004) DOE Joint Genome Institute, 2800 Mitchell
COMMENT          Drive, Walnut Creek, CA 94598, USA
                On Nov 12, 2004 this sequence version replaced gi:54697207.
                Draft Sequence Produced by DOE Joint Genome Institute
                www.jgi.doe.gov
                Finishing Completed at Stanford Human Genome Center
                www.sbgc.stanford.edu
                Quality: Phrap Quality >=40 100% of Sequence;
                Estimated Total Number of Errors is 0.
FEATURES         Location/Qualifiers
source           1..163878
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                 /mol_type="genomic DNA"
                 /db_xref="taxon:7739"
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ORIGIN
Query Match      66.7%; Score 20; DB 2; Length 163878;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY  3  GGCUACGCGTAGAGCAUCATGATCCUGT 30
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Db   68124  GGTACTCGTAGATCAGCATCCTGT 68151

RESULT 12
AC155516/c
LOCUS      AC155516.2 172391 bp      DNA      linear      HTG 25-JAN-2005
DEFINITION Zea mays strain B73 clone ZMMBbc0059P07, *** SEQUENCING IN PROGRESS
ACCESSION  AC155516
VERSION     AC155516.2 GI:58082376
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 172391)
AUTHORS   Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
            Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
            Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
            Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
            Quackenbush, J.
            Consortium for Maize Genomics - BAC skim sequencing and assembly
            Unpublished
            2 (bases 1 to 172391)
            Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
            Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
            Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
            Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
            Quackenbush, J.
            Direct Submission
            Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
            9712 Medical Center Dr, Rockville, MD 20850
            3 (bases 1 to 172391)
            Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
            Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
            Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
            Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
            Quackenbush, J.
            Direct Submission
            Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
            9712 Medical Center Dr, Rockville, MD 20850
            On Jan 25, 2005 this sequence version replaced gi:57863037.
            ----- Trace submission

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Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, C., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramaaam, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (23-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 174912)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wang, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckghalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, C., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramaaam, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (16-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 16, 2004 this sequence version replaced gi:48717645.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (<http://pgir.rutgers.edu>)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information
Center project name: L25606
Center clone name: 36_A.1

----- Consensus Information
This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (<http://www.ncbi.nlm.nih.gov/traces/trace.fcgi?>). An exact list of reads used in this assembly are available at <http://www.broad.mit.edu/annotation/plants/maize/randomclones.html>.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 28758: contig of 28758 bp in length
28759 28858: gap of 100 bp
28859 174912: contig of 146054 bp in length.

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ORIGIN
Query Match 66.7%; Score 20; DB 14; Length 174912;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGGCUACGCGTAGAGCAUCATGATCCUG 29
DB 25981 AGACAACGCGTCGAGCATATTATGATGCTG 26008

RESULT 14
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LOCUS
DEFINITION AC155574 181826 bp DNA linear HTG 25-JAN-2005
Zea mays strain B73 clone ZMMBGC017711, *** SEQUENCING IN PROGRESS
***, 33 unordered pieces.
AC155574
AC155574.2 GI:58082433
VERSION
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 181826)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
Consortium for Maize Genomics - BAC skim sequencing and assembly
Unpublished
2 (bases 1 to 181826)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 181826)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863095.
----- Trace submission

[illegible]

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ORIGIN					
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ORIGIN

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Best Local Similarity 87.0%; Pred. No. 5.5e+02;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      7  ACGCGTAGAGCAUCATGATCCUG 29
Db      2363 ACGGTACGATCATGATCCCG 2385
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Job time : 1732 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 15:08:49 ; Search time 2518 Seconds
(without alignments)
557.431 Million cell updates/sec

Title: US-10-791-367-1

Perfect score: 30

Sequence: 1 caggcuacgctagagcaucatgatccctg 30

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_hrc.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_est7.*

9: gb_gss1.*

10: gb_gss2.*

11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20.6	68.7	526	7	CO786247	CO786247 BL285D.D0
C 3	20.6	68.7	683	1	AU170138	AU170138 AU170138
C 4	20.6	68.7	724	3	BJ716634	BJ716634 BJ716634
C 5	20.4	68.0	451	5	BX306829	BX306829 BX306829
C 6	20.4	68.0	501	9	CE251821	CE251821 tigr-gss-
C 7	20.4	68.0	521	9	AQ405865	AQ405865 HS5043.B
C 8	20.4	68.0	631	1	AJ745356	AJ745356 AJ745356
C 9	20.4	68.0	639	5	CA058120	CA058120 ssalrga51
C 10	20.4	68.0	759	9	CC494201	CC494201 CH240_329
C 11	20.4	68.0	1332	8	DN711869	DN711869 CLJ97-H05
C 12	20.4	68.0	1351	8	DN686483	DN686483 CGX47-C07
C 13	20.4	68.0	1372	8	DN711868	DN711868 CLJ97-H05
C 14	20.4	68.0	1413	8	DN686482	DN686482 CGX47-C07
C 15	20.4	68.0	1669	10	CL640951	CL640951 CH213-1N0
C 16	20.2	67.3	362	10	CZ914756	CZ914756 4013008E0
C 17	20.2	66.7	582	8	DN407618	DN407618 LIB4006-0
C 18	20.2	66.7	697	9	CC145434	CC145434 ZMMBB000
C 19	20.2	66.7	820	5	BU745550	BU745550 CH1#010.E
C 20	20.2	66.7	862	9	CC982446	CC982446 ZUAES75FH
C 21	20.2	66.7	916	5	BU745549	BU745549 CH1#010.E
C 22	19.6	65.3	393	5	BX565471	BX565471 BX565471

C 23	19.6	65.3	500	5	BX558657	BX558657
C 24	19.6	65.3	520	7	CO294995	CO294995
C 25	19.6	65.3	573	5	BX562437	BX562437
C 26	19.6	65.3	581	5	BX556173	BX556173
C 27	19.6	65.3	591	5	BX568347	BX568347
C 28	19.6	65.3	597	5	BX568861	BX568861
C 29	19.6	65.3	637	5	BX551247	BX551247
C 30	19.6	65.3	837	1	A1404024	A1404024 GH23607.5
C 31	19.6	65.3	1153	10	AG385831	AG385831 Mus muscu
C 32	19.4	64.7	414	9	AQ181478	AQ181478 HS 3219.A
C 33	19.4	64.7	713	9	BH035476	BH035476 RPCI-24-2
C 34	19.4	64.7	768	9	CC934167	CC934167 ZMMBB054
C 35	19.4	64.7	777	3	BJ566348	BJ566348
C 36	19.4	64.7	792	5	BQ363359	BQ363359 603790407
C 37	19.4	64.7	810	9	AQ875939	AQ875939 V131C6.mt
C 38	19.4	64.7	840	9	AQ251296	AQ251296 T30110-Sp
C 39	19.4	64.7	5463	4	CR858601	CR858601 Pongo pyg
C 40	19.2	64.0	466	2	BE125931	BE125931 DGI_59.G0
C 41	19.2	64.0	585	8	DR063891	DR063891 ip71e04.g
C 42	19.2	64.0	654	2	BF528338	BF528338 602044251
C 43	19.2	64.0	666	9	BZ335768	BZ335768 hz26905.g
C 44	19.2	64.0	724	10	CW487118	CW487118 fssb001f2
C 45	19.2	64.0	772	9	BZ628162	BZ628162 ih58c10.b

ALIGNMENTS

RESULT 1
BW778170/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BW778170 389 bp mRNA linear EST 10-AUG-2005
BW778170 Amphioxus Branchiostoma floridae unpublished cDNA library,
gastrula whole animal Branchiostoma floridae cDNA clone bbga048o03
5', mRNA sequence.
BW778170
BW778170.1 GI:66380664
EST.
Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
1 (bases 1 to 389)
Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
Expressed genes in Branchiostoma floridae
Unpublished (2005)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this EST or if you have any
questions, please send an e-mail to Nori Satoh
(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
(yutaka@ascidian.zool.kyoto-u.ac.jp).

FEATURES

source

Location/Qualifiers
1..389
/organism="Branchiostoma floridae"
/mol_type="mRNA"
/db_xref="taxon:7739"
/clone="bbga048o03"
/tissue_type="whole animal"
/dev_stage="gastrula"
/clone_lib="Amphioxus Branchiostoma floridae unpublished
cDNA library, gastrula whole animal"

ORIGIN

Query Match 68.7%; Score 20.6; DB 5; Length 389;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 AGGCUACGGTAGAGCAUCAATGATCCU 28

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||||:|||||:|||||:|||||:|||||:
195 AGGCTACAGTAGAGCAACTTGATGCT 169

RESULT 2
LOCUS       CO786247
DEFINITION  BL285D D03 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
              cDNA 5' similar to Unknown (protein for MGC:89099) (Xenopus
              tropicalis), mRNA sequence.
ACCESSION   CO786247
VERSION     CO786247.1 GI:51002227
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
ORGANISM    Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1 (bases 1 to 526)
AUTHORS    Habermann,B., Bebin,A.G., Herklitz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,B.M.
TITLE      An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
JOURNAL     Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauserstrasse 108, 01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL285D row: 03 Column: D
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
            Location/Qualifiers
                1..526
                /organism="Ambystoma mexicanum"
                /mol_type="mRNA"
                /db_xref="taxon:8296"
                /tissue_type="Tail Blastema"
                /cell_type="regenerating tail blastema"
                /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
                /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
                Unnormalized cDNA plasmid library prepared by Invitrogen.
                Size fractionated mRNA was polydT primed and cloned into
                NotI-SalI site of pCMVSPORT6. Bacterial host is
                EMDH10B-TONA. Average insert size is 1.67 kB.
                TAG_LIB=6DAXBL"

ORIGIN
Query Match      68.7%; Score 20.6; DB 7; Length 526;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4  GCUACGCTAGAGCAUCATGATCCUCT 30
          |||:|||||:|||||:|||||:
Db      230 GCTACACGAGAGCGCGCATGATCCTGT 256

FEATURES
source
LOCUS       AU170138
DEFINITION  AU170138 OI-br-ad cDNA Oryzias latipes cDNA clone br5670, mRNA
              sequence.
ACCESSION   AU170138
VERSION     AU170138.1 GI:12592209
KEYWORDS    EST.
SOURCE      Oryzias latipes (Japanese medaka)
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

ORIGIN
Query Match      68.7%; Score 20.6; DB 7; Length 526;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4  GCUACGCTAGAGCAUCATGATCCUCT 30
          |||:|||||:|||||:|||||:
Db      230 GCTACACGAGAGCGCGCATGATCCTGT 256

FEATURES
source
LOCUS       AU170138
DEFINITION  AU170138 OI-br-ad cDNA Oryzias latipes cDNA clone br5670, mRNA
              sequence.
ACCESSION   AU170138
VERSION     AU170138.1 GI:12592209
KEYWORDS    EST.
SOURCE      Oryzias latipes (Japanese medaka)
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

ORIGIN
Query Match      68.7%; Score 20.6; DB 1; Length 683;
Best Local Similarity 74.1%; Pred. No. 2.7e+02;
Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      4  GCUACGCTAGAGCAUCATGATCCUCT 30
          |||:|||||:|||||:|||||:
Db      483 GCTACACGAGAGCGCATGATGACCTGT 509

FEATURES
source
LOCUS       BJT16634
DEFINITION  BJT16634 MF01FFA cDNA Oryzias latipes cDNA clone MF01FFA013h19 3',
              mRNA sequence.
ACCESSION   BJT16634
VERSION     BJT16634.1 GI:45257475
KEYWORDS    EST.
SOURCE      Oryzias latipes (Japanese medaka)
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
            1 (bases 1 to 724)
            Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
            Medaka EST Project in Takeda's lab
            Unpublished (2001)
            Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yatai Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
                1..724
                /organism="Oryzias latipes"
                /mol_type="mRNA"
                /strain="Hd-rR"
                /db_xref="taxon:8090"
                /clone="MF01FFA013h19"
                /sex="mixture of female and male"
                /tissue_type="whole embryo"
                /dev_stage="fry stage 40"
                /clone_lib="MF01FFA cDNA"

ORIGIN

```

Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
 1 (bases 1 to 683)
 Mita,K., Ishikawa,Y. and Yamauchi,M.
 Establishment of cDNA database of medaka, Oryzias latipes
 Unpublished (2001)
 Contact: Mita K
 Genome Research Group
 National Institute of Agrobiological Sciences
 Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
 Tel: 81-29-838-6120
 Fax: 81-29-838-6121
 Email: kmita@nias.affrc.go.jp
 Method: uni-directional sequence direction: sequenced from T3 primer
 (5' -> 3').

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

ORIGIN

Query Match 68.7%; Score 20.6; DB 1; Length 683;
 Best Local Similarity 74.1%; Pred. No. 2.7e+02;
 Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCUACGCTAGAGCAUCATGATCCUCT 30
 |||:|||||:|||||:|||||:
 Db 483 GCTACACGAGAGCGCATGATGACCTGT 509

FEATURES

source

LOCUS BJT16634/c
 DEFINITION BJT16634 MF01FFA cDNA Oryzias latipes cDNA clone MF01FFA013h19 3',
 mRNA sequence.

ACCESSION BJT16634
 VERSION BJT16634.1 GI:45257475
 KEYWORDS EST.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.

1 (bases 1 to 724)
 Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
 Medaka EST Project in Takeda's lab
 Unpublished (2001)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yatai Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES

source

LOCUS AU170138
 DEFINITION AU170138 OI-br-ad cDNA Oryzias latipes cDNA clone br5670, mRNA

sequence.
 ACCESSION AU170138
 VERSION AU170138.1 GI:12592209
 KEYWORDS EST.

SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;


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Query Match      68.7%; Score 20.6; DB 3; Length 724;
Best Local Similarity 74.1%; Pred. No. 2.7e+02;
Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCUACGCGTAGAGCAUCATGATCCUGT 30
Db 605 GCTACAGAGAGCATCATGAGCCGTGT 579

RESULT 5
BX306829 451 bp mRNA linear EST 11-MAY-2004
LOCUS BX306829 tcay Oncorhynchus mykiss cDNA clone tcay001/b.e.20 3prtm,
DEFINITION mRNA sequence.
ACCESSION BX306829
VERSION BX306829.2 GI:40223548
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 451)
AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
JOURNAL Unpublished (2003)
COMMENT On Apr 7, 2003 this sequence version replaced gi:29587474.
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0017 row: e column: 20
Seq primer: M13F.

FEATURES             Location/Qualifiers
     source
     1..451
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /clone="tcay001/b.e.20"
     /tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
     /dev_stage="from embryos to adults"
     /lab_host="DH10B"
     /clone_lib="tcay"
     /note="Vector: pTT73D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcay); Clone distribution :
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouv-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match      68.0%; Score 20.4; DB 5; Length 451;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 21; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
Db 263 CAGGCTAATGTTAGAAATCATGATCCTTT 234

RESULT 7
AQ405865/c 521 bp DNA linear GSS 13-MAR-1999
LOCUS HS_5043_B2_D11_T7 RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=619 Col=22 Row=H, genomic survey sequence.
ACCESSION AQ405865
VERSION AQ405865.1 GI:4415853
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

tigr-gss-dog-17000335914549 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE251821
VERSION CE251821.1 GI:35948893
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 501)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: Shotgun.
Location/Qualifiers
     source
     1..501
     /organism="Canis familiaris"
     /mol_type="genomic DNA"
     /strain="Standard Poodle"
     /db_xref="taxon:9615"
     /clone_lib="Dog Library"
     /note="Site 1: BatXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match      68.0%; Score 20.4; DB 9; Length 501;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 21; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
Db 263 CAGGCTAATGTTAGAAATCATGATCCTTT 234

RESULT 7
AQ405865/c 521 bp DNA linear GSS 13-MAR-1999
LOCUS HS_5043_B2_D11_T7 RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=619 Col=22 Row=H, genomic survey sequence.
ACCESSION AQ405865
VERSION AQ405865.1 GI:4415853
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

```


Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@shgc.stanford.edu
 Plate: 97
 High quality sequence stop: 872.
 Location/Qualifiers
 1..1332
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Bitrufjordur marine sticklebacks, Iceland"
 /db_xref="taxon:69293"
 /clone="CLJ97-H05"
 /sex="mixed male and female"
 /tissue_type="whole larva"
 /dev_stage="21 day old larvae collected at Swarup Stage 30
 (J. Embryol. Exp. Morphol 6: 373-383,1958)"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CLJ"
 /note="Vector: Express 1: Total and poly A+ RNA was
 isolated from the indicated stickleback tissue, and a cDNA
 library was constructed in the Express 1 plasmid vector by
 Open Biosystems. First strand cDNA synthesis was primed
 with an 54 bp linker primer containing an oligodT sequence
 preceded by a synthetic NotI site (first strand primer:
 5'-GACTAGTTCATGACGCGAGCGCGCC(T)25-3'). Following
 second strand synthesis, cDNAs were made blunt at the end
 corresponding to the original 5 prime end of mRNA, and
 cloned directionally into the NotI and EcoRV sites of
 Express 1. Note that the EcoRV site is typically destroyed
 in the blunt end cloning, leaving a junction of the form
 'xxxATC'(where is ATC is the second half of the EcoRV
 site, and xxx is derived from the cDNA sequence). A map of
 the Express 1 vector is available at:
 http://www.openbiosystems.com/cdna_library.construction.f
 a.php#8 The primary library was transformed and amplified
 in DH10B (T1 phage resistant) bacteria. Clones available
 from Open Biosystems:
 http://www.openbiosystems.com/stickleback"

ORIGIN
 Query Match 68.0%; Score 20.4; DB 8; Length 1332;
 CGX47-C07 70.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CAGGCUACGGGTAGCAUCATGATCCUOT 30
 ||||| ||||| ||||| ||||| ||||| |||||
 DB 811 CGGCGCTACAAGCAGACATCATCGCGCTGT 840

RESULT 12
 DN686483
 LOCUS
 DEFINITION
 CGX47-C07 5', mRNA sequence.
 DN686483 1351 bp mRNA linear EST 30-MAR-2005
 CGX47-C07 5', mRNA sequence.
 DN686483 1 GI:62035850
 DN686483.1
 Gasterosteus aculeatus (three spined stickleback)
 Gasterosteus aculeatus
 EST.
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.
 1 (bases 1 to 1351)
 KINGSELEY,D.M., PEICHEL,C., BALABHADRA,S., GRIMWOOD,J., DICKSON,M.,
 SCHMUTZ,J. and MYERS,R.M.
 Expressed sequence tags from Gasterosteus aculeatus
 Unpublished (2003)
 Contact: Grimwood, Jane

Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@shgc.stanford.edu
 Plate: 47
 High quality sequence start: 15
 High quality sequence stop: 782.

FEATURES

source
 1. .1413
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CGX47-C07"
 /sex="mixed male and female"
 /tissue_type="eyes"
 /dev_stage="adult"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CGX"

/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCGATCGAGCGCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxATC'(where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 68.0%; Score 20.4; DB 8; Length 1413;
 Best Local Similarity 70.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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 DB 673 CGGGCTACAGCAGCATCATGCCCTGT 644

RESULT 15

CL640951
 LOCUS CH213-IN08.T7 CH213 Gasterosteus aculeatus genomic clone CH213-IN08
 DEFINITION 5', genomic survey sequence.
 CL640951
 CL640951.1 GI:49660375
 GSS.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gasterosteus aculeatus (three spined stickleback)
 Gasterosteus aculeatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1669)
 Kingsley, D., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
 Expressed sequence tags from *Gasterosteus aculeatus*
 Unpublished (2004)
 Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Avenue, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801

Email: jane@shgc.stanford.edu
 Plate: 1
 Class: BAC ends
 High quality sequence start: 35
 High quality sequence stop: 462.
 Location/Qualifiers
 1. .1669

/organism="Gasterosteus aculeatus"
 /mol_type="genomic DNA"
 /strain="Salmon River"
 /db_xref="taxon:69293"
 /clone="CH213-IN08"
 /sex="Mixed"
 /cell_type="Blood"
 /clone_lib="CH213"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (<http://cegs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm)."

ORIGIN

Query Match 68.0%; Score 20.4; DB 10; Length 1669;
 Best Local Similarity 70.0%; Pred. No. 3.7e+02;
 Matches 21; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
 |||||
 DB 493 CGGGCTACAGCAGCATCATGCCCTGT 522

Search completed: January 8, 2006, 17:06:47
 Job time : 2521 secs

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